AMENDMENTS TO THE SPECIFICATION

On page 15, line 26 after "GMTCXXC" please insert (SEQ ID NO: 15)

On page 16, line 1 after "DKTGT" please insert (SEQ ID NO: 16)

On page 16, line 2 after "TGDN" please insert (SEQ ID NO: 17)

On page 16, line 3 after "MXGDXNDX" please insert (SEQ ID NO: 18)

On page 15, line 28 after "TGES/A" please insert (SEQ ID NO 19, 20)

In context, the paragraph containing these changes would read:

In order to manufacture DNA chip for diagnosis of mutations causing Wilson disease, the mutations to be interrogated were selected. For successful diagnosis of Wilson disease, the informations about nucleotide and amino acid sequence of ATP7B protein which is the cause of Wilson disease, were obtained from NCBI(National Center for Biotechnology Information)-affiliated gene databases, GenBank and OMIN(Online Medelian Inheritance in Man), as well as informations on the allelic variants of the disease were obtained. Furthermore, based on above-obtained amino acid sequence information and the report obtained from a published literature(see: Kim, E.K., Ph.D. thesis, KAIST, 1999), ATP7B protein was examined for functional motifs. A functional motif of a protein is a short stretch of amino acid sequence representing a particular function of the protein, and following functional motifs have been found in the ATP7B protein; a copper-binding motif GMTCXXC (SEQ ID NO: 15) at the N-terminal side of the protein, a transduction domain which has homology to TGES/A (SEQ ID NO 19, 20) amino acid sequence, a cation channel motif CPC, a phosphate domain DKTGT (SEQ ID NO: 16), an ATP bindig domain TGDN (SEQ ID NO: 17) at the C-terminal side of the protein, and a hinge region MXGDXNDX (SEQ ID NO: 18), wherein X refers to any amino acid not a particular amino acid. According to HGMD(Human Gene Mutation Database), Wilson disease has been known to be caused by 12 types of variant ATP7B protein encoded by 12 types of gene with substitution mutation in functionally important domains including phosphate domain, ATP binding domain and hinge domain, and among the mutations found in 12 types of protein, Asn1270 mutation has been reported to be found in Korean Wilson disease patients. Therefore, the present inventors have selected, as mutations to be interrogated, 14 substitution mutations leading 14 variant proteins including Arg778Leu(see: Kim, E. K., *et al, Hum. Mutat.*, 11:275-278, 1998) which represented 37.5% of Wilson disease alleles in Korean patients and

His1069Gln(see: Payne, A., *et al, Proc. Natl. Acad. Sci.*, USA, 95:10854-10859, 1998) which found in patients in western population with considerable frequency.

Please cancel from the Application the Sequence Listing submitted with the Response to Notice to Comply of Jan 3, 2002. Please substitute therefore the attached Replacement Sequence Listing pages. Please consecutively renumber all pages following the canceled Sequence Listing.